

APPLICANT(S): CAPPOLA, Thomas. *et al.*

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AMENDMENTS TO THE CLAIMS

Please amend the claims as follows:

1. (Currently amended) A method for predicting a cardiac transplant rejection in a human subject, comprising: collecting a blood sample from said subject; determining a gene expression profile in said sample subject, wherein said gene expression profile comprises increased expression of at least 4 genes as compared to a standard, and diminished expression of at least one gene, as compared to said standard, wherein one of said at least 4 genes is an ubiquinol-cytochrome c reductase binding protein (UQCRB), thereby predicting said transplant rejection in said subject.
2. (Currently amended) The method of claim 1, wherein said increased expression is of at least four genes or more of a comprise an ubiquinol-cytochrome c reductase binding protein (UQCRB), basic transcription factor 3 (BTF3), suppression of tumorigenicity 13 (ST13), and cullin 4A (CUL4A), TERF2IP, ARRB2, or NPEPPS gene.
3. (Original) The method of claim 1, wherein increased expression of said genes, are increased by at least 30% as compared to said standard.
4. (Currently amended) The method of claim 1, wherein said at least one gene with diminished expression is a ARRB2, NPEPPS, PIGB, APC, BCL7A, EDG4, IL17R, PGF, NFAT5, BIRC1, LHRB3, TM6SF2, CASP8 and FADD-like apoptosis regulator (CFLAR), SOD2, SLC16A3 or SCD4 gene, or a combination thereof.
5. (Currently amended) The method of claim 1, wherein said diminished expression of said gene, is diminished by at least 25% compared with said standard.

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6. (Original) The method of claim 1, wherein said at least one gene with diminished expression does not encode for a known protein.
7. (Original) The method of claim 1, wherein said gene expression profile further comprises a nucleic acid whose expression is diminished, wherein said nucleic acid does not encode for a functional protein.
8. (Original) The method of claim 7, wherein said nucleic acid is an expressed sequence tag (EST).
9. (Currently amended) The method of claim 8, wherein said expressed sequence tag comprises a nucleic acid sequence corresponding or homologous to SEQ ID. No.: s. 4—12.
10. (Original) The method of claim 1, wherein said transplant is cardiac.
11. (Currently amended) The method of claim 10, wherein said transplant is a[[n]] cardiac allograft.
12. (Original) The method of claim 1, wherein determining said gene expression profile is conducted via the use of a microarray.
13. (Currently amended) A method for identifying a candidate for successful cardiac allograft transplantation in a human subject comprising: collecting a blood sample from said subject; determining a gene expression profile in said sample, wherein said gene expression profile comprises increased expression of at least 1 gene as compared with a standard, concurrent with diminished expression of at least 4 genes compared with said standard, wherein one of said at least 4 genes is an ubiqinol-cytochrome c reductase binding protein (*UQCRB*), thereby identifying said candidate.

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14. (Currently amended) The method of claim 13[[5]], wherein said underexpressed genes comprise are at least any four of an ubiquinol-cytochrome c reductase binding protein (UQCRB), basic transcription factor 3 (BTF3), suppression of tumorigenicity 13 (ST13), and cullin 4A (CUL4A), TERF2IP, ARRB2, or NPEPPS.
15. (Currently amended) The method of claim 13[[5]], wherein said underexpressed genes, are underexpressed by at least 30% compared with said standard.
16. (Currently amended) The method of claim 13, wherein said gene with increased expression is ARRB2, NPEPPS, PIGB, APC, BCL7A, EDG4, IL17R, PGF, NFAT5, BIRC1, LILRB3, TM6SF2, cullin 4A (CFLAR), SOD2, SLC16A3, SCD4 or combination thereof.
17. (Currently amended) The method of claim 16[[5]], wherein increased expression of said gene, is increased by at least 25% compared with standard.
18. (Currently amended) The method of claim 16[[5]], wherein said gene with increased expression does not encode for a known protein.
19. (Withdrawn) A medium having disposed thereon a cRNA of UQCRB, BTF3, ST13, CUL4A, TERF2IP, ARRB2, NPEPPS, ARRB2, NPEPPS, PIGB, APC, BCL7A, EDG4, IL17R, PGF, NFAT5, BIRC1, LILRB3, TM6SF2, CFLAR, SOD2, SLC16A3 or SCD4.
20. (Withdrawn) The medium of claim 19, wherein the medium is machine readable.
21. (Withdrawn) The medium of claim 20 in the form of a microarray chip.

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22. (Withdrawn) The medium of claim 19, wherein the oligonucleotide is detectably labeled.
23. (Withdrawn) A kit for predicting transplant tolerance, said kit comprising a microarray comprising immobilized nucleic acids, wherein said nucleic acids exhibit complementarity to a *UQCRB*, *BTF3*, *ST13*, *CUL4A*, *TERF2IP*, *ARRB2*, *NPEPPS*, *ARRB2*, *NPEPPS*, *PIGB*, *APC*, *BCL7A*, *EDG4*, *IL17R*, *PGF*, *NFAT5*, *BIRC1*, *LILRB3*, *TM6SF2*, *CFLAR*, *SOD2*, *SLC16A3* and *SCD4* gene, or fragments thereof.
24. (Withdrawn) The kit of claim 23, further comprising immobilized nucleic acid whose sequence is complimentary to that set forth in SEQ ID Nos. 1 - 12.
25. (Withdrawn) The kit of claim 23, further comprising reagents for processing a biological sample and isolating mRNA from said sample.
26. (Withdrawn) The kit of claim 25, further comprising an agent which labels said mRNA isolated from said biological sample..
27. (Withdrawn) The kit of claim 23, further comprising instructions for use in determining the expression of said genes in a biological sample.
28. (Withdrawn) The kit of claim 27, further comprising directions for correlating said gene expression with a likelihood of transplant tolerance.
29. (Withdrawn) The kit of claim 23, wherein said kit further comprises a buffering agent, a preservative, or a protein stabilizing agent.
30. (Withdrawn) The kit of claim 23, wherein said kit further comprises an enzyme or a substrate.